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GENETIC VARIATION IN SUSCEPTIBILITY OF WESTERN
WHITE PINE TO NEEDLE BLIGHT

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ABSTRACT

Ten clones of western white pine differed in their susceptibility to white pine needle blight. Two clones were significantly less infected than the average and two clones were significantly more infected than the average. This variability suggests a simple inheritance, maybe just one or two genes.

KEYWORDS: western white pine, white pine needle blight, genetic variability, disease resistance

Needle blight, a periodically occurring disease of western white pine associated with wet summers, generally affects needles and buds of the lower crown. Under severe conditions, however, most of the crown becomes diseased and death often occurs. Shaw and Leaphart (1960) isolated several organisms from needle-blighted trees. But they considered a *Lecanosticta* species to be the causal organism because it was consistently associated with the disease.

The last severe outbreak was in the late fifties-early sixties. Recent wet springs and summers have led to severe infection in a clonal seed orchard of western white pine resistant to blister rust (*Cronartium ribicola*). Though not welcome, the severe infection presented an opportunity of documenting genetic variation in susceptibility to needle blight.

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MATERIALS AND METHODS

The seed orchard was established in 1960 at Sandpoint, Idaho (Bingham and others 1963). Clones were selected for their high levels of rust resistance on the basis of progeny test results. Since rust resistance was the only characteristic selected, variation in all other characters can be considered to be random. The seed orchard was designed to provide an experimental area for testing various seed orchard procedures, to determine the long term effects of grafting, and to provide materials for which genetic variation could be documented, as well as for production of resistant seed.

The seed orchard consists of 13 clones arranged in a randomized block design with- in 14 blocks. Some blocks and clones were incomplete; thus, only a portion of the seed orchard, complete blocks (9) and those clones having at least one ramet per block (10), was used in the analysis (table 1).

The tree crowns were placed into one of three categories: (1) no infection; (2) up to 30 percent of the crown infected; (3) 30 to 60 percent of the crown infected. There were no trees in the sample with more than 60 percent of the crown infected. Since symptoms are most noticeable in the fall, the data were taken in November (1975). The data were analyzed by category, i.e., 1, 2, or 3.

Independence of blocks and clones was determined via a 9 by 10 chi-square table (Snedecor 1966). The sum of all ramets/clone/block comprised the observed value. For example, the eight ramets of clone 17, block 1, were rated 1,2,1,2,3,1,2,1 for a sum of 13. The expected value (14.23) was the product of the mean for a block (1.67) and a clone (1.79) divided by the total mean (1.68) multiplied by the number of ramets/ clone/block (8). Differences among clones and blocks were determined by comparing the contribution of each to the overall chi-square for blocks and clones.

Table 1.-Number of ramets per clone and block

Clone	Block										Total
	1	2	3	4	5	6	10	11	13		
17	8	9	10	9	8	8	8	9	8	77	
19	9	10	10	8	9	9	10	10	9	84	
20	9	7	8	8	7	8	7	8	3	65	
21	7	4	5	7	4	3	6	2	6	44	
22	10	8	8	8	10	10	8	9	10	81	
24	7	10	6	9	9	8	7	6	10	72	
37	3	8	7	6	9	9	9	9	7	67	
45	5	9	7	5	7	7	8	6	7	61	
58	1	5	8	6	2	2	9	6	4	43	
65	4	1	4	2	2	4	5	3	4	29	
Total	63	71	73	68	67	68	77	68	68	623	

RESULTS, DISCUSSION, AND CONCLUSIONS

The interaction chi-square of clones and blocks was not significant (table 2). The among-block variation was also nonsignificant but the among-clone chi-square was highly significant. The contribution of each clone to the total clone chi-square is listed in table 3.

The orchard is located on a flat area that was once a pasture. The trees are spaced at 20 by 20 ft and they were only 20 to 30 ft tall in 1975. It is not surprising, therefore, that there was no difference among the blocks.

On the other hand, the highly significant difference among clones, especially when considering the number of ramets per clone, shows that there is a strong genetic influence of the host on the parasite's ability to infect various white pine trees. Although the mechanism(s) of resistance and mode of inheritance are not revealed by our test, two clones had high resistance (19 and 24) and two clones had low resistance (65 and 37) with the remaining close to the mean, which suggests a simple genetic pattern.

Different levels of infection of individuals and stands, by diseases in general, are nearly always considered to be due to environmental causes. Infection levels of white pine needle blight are frequently higher at the edges of stands. Nonetheless, within this environmentally induced variation there is frequently, possibly always, an underlying genetic factor that also affects the observed variation. Successful management practices are developed only by knowing all the causes of variation--do not forget the genetic component.

Table 2.--Observed and expected values of western white pine infected with needle blight

Clone	Block										\bar{x}	Total
	1	2	3	4	5	6	10	11	13			
17	13/14.23*	16/17.15	17/17.0	15/15.53	14/14.15	15/14.06	17/14.75	16/16.78	15/14.41	1.79	138/129.36	
19	9/10.56	11/12.57	12/11.24	8/9.10	10/10.49	10/10.43	14/12.14	12/12.39	13/10.68	1.18	99/141.12	
20	14/15.66	14/13.05	12/13.33	13/13.50	13/12.10	15/13.75	13/12.61	17/14.58	3/5.28	1.75	114/109.2	
21	9/9.46	7/6.09	9/6.81	12/9.66	4/5.65	3/4.21	9/8.84	2/2.98	8/8.63	1.43	63/75.92	
22	19/19.1	15/15.26	12/13.64	11/13.81	16/17.69	17/17.58	15/14.75	19/16.78	21/18.0	1.79	145/136.05	
24	10/8.70	14/13.32	6/7.14	13/10.85	11/11.12	8/9.82	7/9.01	7/7.81	14/12.6	1.25	90/120.96	
37	8/7.25	23/20.71	16/16.20	18/14.06	21/21.61	21/21.48	18/22.52	22/22.78	16/17.11	2.43	163/112.56	
45	11/8.15	15/15.73	11/10.93	7/7.91	12/11.34	9/11.28	12/13.51	9/10.25	14/11.55	1.64	100/102.48	
58	2/1.59	9/8.52	12/12.19	9/9.26	4/3.16	2/3.14	17/14.83	8/10.00	6/6.44	1.60	69/72.24	
65	10/9.30	3/2.49	10/8.91	4/4.51	6/4.62	12/9.19	11/12.05	7/7.31	5/9.42	2.34	68/48.72	
\bar{x}	1.67	1.79	1.60	1.62	1.66	1.65	1.73	1.75	1.69	1.68		
Total	105/ 105.84	127/ 119.28	117/ 112.64	110/ 114.24	111/ 112.56	112/ 114.24	133/ 129.36	119/ 114.24	115/ 114.24		1,049	

χ^2 Blocks x Clones = 19.97 with 76 d.f.

χ^2 Blocks = 1.21 with 8 d.f.

χ^2 Clones = 53.92** with 9 d.f.

*Expected = \bar{x} clone (1.79) X \bar{x} block (1.67)/ \bar{x} total (1.68) X ramet number (8) = 14.23.

**Denotes significant deviation from the mean at 1 percent probability, 9 degrees of freedom.

Table 3.--*Contribution of individual clones to chi-square and the level of needle blight infection of western white pine*

	Clones									
	: 19	: 24	: 17	: 20	: 21	: 22	: 45	: 58	: 65	: 37
χ^2	12.57	7.92	0.58	0.21	1.61	0.59	0.06	0.15	7.62	22.6
Infection level	Low	Low	- - - - -	- - - - -	- - - - -	Medium	- - - - -	- - - - -	High	High

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